

SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> Shiga-like toxin vaccine

<130> 2003.006

<160> 4

<170> PatentIn version 3.2

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<212> DNA

<213> Escherichia coli

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<221> CDS

<222> (1)..(954)

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Phe Ser Ser Val Ser Tyr Ser Gln Glu Phe Thr Ile Asp Phe Ser Thr	
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caa caa agt tat gta tct tcg tta aat agt ata cgg aca gtg ata tcg	144
Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser	
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acc cct ctt gaa cat ata tct cag gga gct aca tcg gta tcc gtt att	192
Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile	
50 55 60	

aat cat aca cca cca gga agt tat att tcc gta ggt ata cga ggg ctt	240
Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu	
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gat gtt tat cag gag cgt ttt gac cat ctt cgt ctg att att gaa cga	288
Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg	
85 90 95	

aat aat tta tat gtg gct gga ttt gtt aat acg aca aca aat act ttc	336
Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Asn Thr Phe	
100 105 110	

tac aga ttt tca gat ttt gca cat ata tca ttg ccc ggt gtg aca act	384
Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr	
115 120 125	

att tcc atg aca acg gac agc agt tat acc act ctg caa cgt gtc gca	432
Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala	
130 135 140	

gcg ctg gaa cgt tcc gga atg caa atc agt cgt cac tca ctg gtt tca	480
Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser	
145 150 155 160	

tca tat ctg gcg tta atg gag ttc agt ggt aat aca atg acc aga gat	528
Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp	
165 170 175	

gca tca aga gca gtt ctg cgt ttt gtc act gtc aca gca gaa gcc tta	576
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Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu			
180	185	190	
cgg ttc agg caa ata cag aga gaa ttt cgt ctg gca ctg tct gaa act		624	
Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr			
195	200	205	
gct cct gtt tat acg atg acg ccg gaa gac gtg gac ctc act ctg aac		672	
Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn			
210	215	220	
tgg ggg aga atc agc aat gtg ctt ccg gag tat cgg gga gag gct ggt		720	
Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly			
225	230	235	240
gtc aga gtg ggg aga ata tcc ttt aat aat ata tca gcg ata ctt ggt		768	
Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly			
245	250	255	
act gtg gcc gtt ata ctg aat tgt gga aat tca tca aga aca atc aca		816	
Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr			
260	265	270	
ggt gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc		864	
Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu			
275	280	285	
agg gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag		912	
Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln			
290	295	300	
tca gag gtt gac ata tat aac aga att cgg gat gaa tta tga		954	
Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu			
305	310	315	
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atgacaagat actatcatat acggaatcga tggcaggcaa aagagaaaatg gttatcatta		1134	
catttaagag cggcgaaaca tttcaggtcg aagtcccgaa cagtcaacat atagactccc		1194	
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Gln Gln Ser Tyr Val Ser Ser Leu Asn Ser Ile Arg Thr Val Ile Ser
35 40 45

Thr Pro Leu Glu His Ile Ser Gln Gly Ala Thr Ser Val Ser Val Ile
50 55 60

Asn His Thr Pro Pro Gly Ser Tyr Ile Ser Val Gly Ile Arg Gly Leu
65 70 75 80

Asp Val Tyr Gln Glu Arg Phe Asp His Leu Arg Leu Ile Ile Glu Arg
85 90 95

Asn Asn Leu Tyr Val Ala Gly Phe Val Asn Thr Thr Asn Thr Phe
100 105 110

Tyr Arg Phe Ser Asp Phe Ala His Ile Ser Leu Pro Gly Val Thr Thr
115 120 125

Ile Ser Met Thr Thr Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala
130 135 140

Ala Leu Glu Arg Ser Gly Met Gln Ile Ser Arg His Ser Leu Val Ser
145 150 155 160

Ser Tyr Leu Ala Leu Met Glu Phe Ser Gly Asn Thr Met Thr Arg Asp
165 170 175

Ala Ser Arg Ala Val Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu
180 185 190

Arg Phe Arg Gln Ile Gln Arg Glu Phe Arg Leu Ala Leu Ser Glu Thr
195 200 205

Ala Pro Val Tyr Thr Met Thr Pro Glu Asp Val Asp Leu Thr Leu Asn
210 215 220

Trp Gly Arg Ile Ser Asn Val Leu Pro Glu Tyr Arg Gly Glu Ala Gly
225 230 235 240

Val Arg Val Gly Arg Ile Ser Phe Asn Asn Ile Ser Ala Ile Leu Gly
245 250 255

Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr
260 265 270

Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu
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Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
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 gtatccgtta ttaatcatac accaccagga agttatattt ccgttaggtat acgagggttt 240
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 gtggctggat ttgttaatac gacaacaaat actttctaca gatttcaga ttttgcacat 360
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 caacgtgtcg cagcgctgga acgttccgga atgcaaatac gtcgtcactc actggttca 480
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 tcagactatac agtcagaggt tgacatatac aacagaattc gggatgaatt atg aat 956
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 Lys Val Lys Cys Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser Leu Tyr
 5 10 15

gca cac gga gct ccc cag act att aca gaa cta tgt tcg gaa tat cgc 1052
 Ala His Gly Ala Pro Gln Thr Ile Thr Glu Leu Cys Ser Glu Tyr Arg
 20 25 30

aac aca caa ata tat acg ata aat gac aag ata cta tca tat acg gaa 1100
 Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr Thr Glu
 35 40 45 50

tcg atg gca ggc aaa aga gaa atg gtt atc att aca ttt aag agc ggc 1148
 Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys Ser Gly
 55 60 65

gaa aca ttt cag gtc gaa gtc ccg ggc agt caa cat ata gac tcc cag 1196
 Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln
 70 75 80

aaa aaa gcc att gaa agg atg aag gac aca tta aga atc aca tat ctg 1244
 Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr Tyr Leu

85

90

95

acc gag acc aaa att gat aaa tta tgt gta tgg aat aat aaa acc ccc 1292
Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys Thr Pro
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Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
35 40 45

Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
50 55 60

Ser Gly Glu Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
65 70 75 80

Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
85 90 95

Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
100 105 110

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn
115 120